PATENT

Our Docket: P-LJ 4494

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Reed and Sato

Serial No.: Pending

Filed: Herewith

For: CD40 ASSOCIATED

PROTEINS

Commissioner for Patents Washington, D.C. 20231

Sir:

Group Art Unit: Unknown Yet

Examiner: Unknown Yet

CERTIFICATE OF MAILING BY "EXPRESS MAIL"

"EXPRESS MAIL" MAILING LABEL NUMBER: EL690155804US

DATE OF DEPOSIT: January 9, 2001

I HEREBY CERTIFY THAT THIS PAPER OR FEE IS BEING DEPOSITED WITH THE UNITED STATES POSTAL SERVICE "EXPRESS MAIL POST OFFICE TO ADDRESSEE" SERVICE UNDER 37 C.F.R. 1.10 ON THE DATE INDICATED ABOVE, AND IS ADDRESSED TO: COMMISSIONER FOR PATENTS WASHINGTON, D.C. 20231.

Lijan Puthuvalıl
(TYPED OR PRINTED NAME OR PERSON MAZLING PAPER OR FEE)
(SIGNATURE OF PERSON MAILING PAPER OR FEE)

REQUEST TO USE COMPUTER READABLE FORM OF SEQUENCE LISTING FROM ANOTHER APPLICATION

The computer readable form in the above-referenced application is identical with that filed in Application Number 08/349,357, filed December 2, 1994. In accordance with 37 CFR 1.821(e), please use the last-filed computer readable form filed in that application as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date for the computer readable form that will be used for the instant application. A paper copy of the Sequence Listing is included in a separately filed preliminary amendment for incorporation into the specification of the instant application.

The Commissioner is hereby authorized to charge payment of any fees associated with the filing submitted herewith or credit any overpayment to Deposit Account No. 03-0370. A duplicate copy of this sheet is enclosed.

Robert T. Ramos

Registration No. 37,915

Respectfully submitted,

Telephone No.: (858) 535-9001 Facsimile No.: (858) 535-8949

CAMPBELL & FLORES LLP 4370 La Jolla Village Drive 7th Floor San Diego, California 92122 **USPTO CUSTOMER NO. 23601**

Date: January 9, 2001

PATENT

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In re application of:) Reed and Sato Group Art Unit: Unknown Yet Serial No.: Pending Examiner: Unknown Yet Filed: Herewith CERTIFICATE OF MAILING BY "EXPRESS MAIL." For: CD40 ASSOCIATED "EXPRESS MAIL" MAILING LABEL NUMBER: EL690155804US PROTEINS DATE OF DEPOSIT: January 9, 2001 I HEREBY CERTIFY THAT THIS PAPER OR FEE IS BEING DEPOSITED WITH THE UNITED STATES POSTAL SERVICE BOX SEQUENCE "EXPRESS MAIL POST OFFICE TO ADDRESSEE" SERVICE UNDER 37 C.F.R. 1.10 ON THE DATE INDICATED ABOVE, AND IS Commissioner for Patents ADDRESSED TO: COMMISSIONER FOR PATENTS WASHINGTON, D.C. 20231. Washington, D.C. 20231 Lijan Puthuvalil
(TYPED OR PRINTED NAME OR PERSON MAILING PAPER OR FEE) Sir:

STATEMENT UNDER 37 C.F.R. § 1.821(f) and (g)

(SIGNATURE

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 CFR § 1.821(c) and (e), respectively, are the I hereby state that the paper and computer readable copies submitted herein are identical to those previously submitted on July 17, 1995, in U.S. Serial No. 08/349,357.

I hereby state that the submission, filed in accordance with 37 C.F.R. § 1.821(g) herein does not include new matter.

Respectfully submitted,

<u>January 9, 2001</u>

Date

Robert T. Ramos

Registration No. 37,915 Telephone: (858) 535-9001 Facsimile: (858) 535-8949

CAMPBELL & FLORES LLP 4370 La Jolla Village Drive Suite 700 San Diego, California 92122 USPTO CUSTOMER NO. 23601

SEQUENCE LISTING



(1)	GENERAL	INFORMATION
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- (i) APPLICANT: Reed, John C. Sato, Takaaki
- (ii) TITLE OF INVENTION: CD40 Associated Proteins
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell and Flores
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 92122
- (V) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (Vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/349,357
 - (B) FILING DATE: 02-DEC-1994
 - (C) CLASSIFICATION:
- (Viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-LJ 1203
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001
 - (B) TELEFAX: (619) 535-8949
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 137..1766
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGAAGTGATG	CCACTTO	GTT	AAG	STCC	CAG I	AGCA	GGTC	AG A	ATCA	GACC:	r Ago	GATCA	GAA	60
ACCTGGCTCC	TGGCTCC	CTGG	CTC	CCTA	CTC '	TTCT	AAGG	AT C	GCTG:	rcc T	AC	AGAAG.	AGA	120
ACTCCTCTTT	CCTAAA	ATG Met 1	GAG Glu	TCG Ser	AGT Ser	AAA Lys 5	AAG Lys	ATG Met	GAC Asp	TCT Ser	CCT Pro	GGC Gly		169

GCG CTG CAG ACT AAC CCG CCG CTA AAG CTG CAC ACT GAC CGC AGT GCT
Ala Leu Gln Thr Asn Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala

15 20 25

GTÅ	Thr	30	Val	Phe	Val	Pro	Glu 35	Gln	GGA Gly	Gly	Tyr	Lys 40	Glu	Lys	Phe		265
Val	Lys 45	Thr	Val	Glu	Asp	Lys 50	Tyr	Lys	TGT Cys	Glu	Lys 55	Cys	His	Leu	Val		313
60	Суз	Ser	Pro	Lys	Gln 65	Thr	Glu	Cys	GGG Gly	His 70	Arg	Ser	Cys	Glu	Ser 75		361
TGC Cys	ATG Met	GCG Ala	GCC Ala	CTG Leu 80	CTG Leu	AGC Ser	TCT Ser	TCA Ser	AGT Ser 85	CCA Pro	AAA Lys	TGT	ACA Thr	GCG Ala 90	TGT Cys		409
CAA Gln	GAG Glu	AGC Ser	ATC Ile 95	GTT Val	AAA Lys	GAT Asp	AAG Lys	GTG Val 100	TTT Phe	AAG Lys	GAT Asp	AAT Asn	TGC Cys 105	TGC Cys	AAG Lys		457
AGA Arg	GAA Glu	ATT Ile 110	CTG Leu	GCT Ala	CTT Leu	CAG Gln	ATC Ile 115	TAT Tyr	TGT Cys	CGG Arg	AAT Asn	GAA Glu 120	AGC Ser	AGA Arg	ggt Gly		505
TGT Cys	GCA Ala 125	GAG Glu	CAG Gln	TTA Leu	ACG Thr	CTG Leu 130	GGA Gly	CAT	CTG Leu	CTG Leu	GTG Val 135	CAT His	TTA Leu	AAA Lys	AAT Asn		553
GAT Asp 140	TGC Cys	CAT His	TTT Phe	GAA Glu	GAA Glu 145	CTT Leu	CCA Pro	TGT Cys	GTG Val	CGT Arg 150	CCT Pro	GAC Asp	TGC Cys	AAA Lys	GAA Glu 155		601
гув	Val	Leu	Arg	160 Lys	Asp	Leu	Arg	Asp	CAC His 165	Val	Glu	Lys	Ala	Cys 170	Lys		649
TAC Tyr	CGG Arg	GAA Glu	GCC Ala 175	ACA Thr	TGC Cys	AGC Ser	CAC His	TGC Cys 180	AAG Lys	AGT Ser	CAG Gln	GTT Val	CCG Pro 185	ATG Met	ATC Ile :		697
Ala	Leu	190	гуз	Hls	GLu	Asp	Thr 195	Asp	TGT Cys	Pro	Сув	Val 200	Val	Val	ser		745
Cys	205	HIS	тЛа	Сув	Ser	Val 210	Gln	Thr	CTC Leu	Leu	Arg 215	Ser	Glu	Gly	Thr		793
220	GIN	GIN	IIe	Lys	Ala 225	His	Glu	Ala	AGC Ser	Ser 230	Ala	Val	Gln	His	Val 235		841
ASII	reu	Leu	тÀг	240	Trp	ser	Asn	Ser	CTC Leu 245	Glu	Lys	Lys	Val	ser 250	Leu		889
Leu	GIN	ASII	255	ser	Val	Glu	Lys	Asn 260	AAG Lys	Ser	Ile	Gln	ser 265	Leu	His		937
ASII	GIII	270	cys	ser	Pne	GIU	11e 275	Glu	ATT Ile	Glu	Arg	Gln 280	Lys	Glu	Met		985
CTT Leu	CGA Arg 285	TAA Asn	AAT Asn	GAA Glu	TCC Ser	AAA Lys 290	ATC Ile	CTT Leu	CAT His	₹TA Leu	CAG Gln 295	CGA Arg	GTG Val	ATA Ile	GAC Asp	1	1033

AGC CAA GCA GAG AAA CTG AAG GAG CTT GAC AAG GAG ATC CGG TCC TTC	1081
Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe 300 315	
CGG CAG AAC TGG GAG GAA GCA GAC AGC ATG AAG AGC AGC GTG GAG TCC Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser 320 325 330	1129
CTC CAG AAC CGC GTG ACC GAG CTG GAG AGC GTG GAC AAG AGC GCG GGG Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly 335 340 345	1177
CAA GTG GCT CGG AAC ACA GGC CTG CTG GAG TCC CAG CTG AGC CGG CAT Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His 350 355 360	1225
GAC CAG ATG CTG AGT GTG CAC GAC ATC CGC CTA GCC GAC ATG GAC CTG Asp Gln Met Leu ser Val His Asp Ile Arg Leu Ala Asp Met Asp Leu 365 370 375	1273
CGC TTC CAG GTC CTG GAG ACC GCC AGC TAC AAT GGA GTG CTC ATC TGG Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp 380 395	1321
AAG ATT CGC GAC TAC AAG CGG CGG AAG CAG GAG GCC GTC ATG GGG AAG Lys lle Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys 400 405 410	1369
ACC CTG TCC CTT TAC AGC CAG CCT TTC TAC ACT GGT TAC TTT GGC TAT Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr 415 420 425	1417
AAG ATG TGT GCC AGG GTC TAC CTG AAC GGG GAC GGG ATG GGG AAG GGG Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly 430 435	1465
ACG CAC TTG TCG CTG TTT TTT GTC ATC ATG CGT GGA GAA TAT GAT GCC Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala 445 450 450	1513
CTG CTT CCT TGG CCG TTT AAG CAG AAA GTG ACA CTC ATG CTG ATG GAT Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp 465 470 475	1561
CAG GGG TCC TCT CGA CGT CAT TTG GGA GAT GCA TTC AAG CCC GAC CCC Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro 480 485 490	1609
AAC AGC AGC TTC AAG AAG CCC ACT GGA GAG ATG AAT ATC GCC TCT Asn ser ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser 495 500 505	1657
GGC TGC CCA GTC TTT GTG GCC CAA ACT GTT CTA GAA AAT GGG ACA TAT Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr 510 520	1705
ATT AAA GAT GAT ACA ATT TTT ATT AAA GTC ATA GTG GAT ACT TCG GAT Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp 525 530 535	1753
CTG CCC GAT CCC T GATAAGTAGC TGGGGAGGTG GATTTAGCAG AAGGCAACTC Leu Pro Asp Pro 540	1806
CTCTGGGGGA TTTGAACCGG TCTGTCTTCA CTGAGGTCCT CGCGCTCAGA AAAGGACCTT	1866
GTGAGACGGA GGAAGCGGCA GAAGGCGGAC GCGTGCCGGC GGGAGGAGCC ACGCGTGAGA	1926

CACCTGACAC	GTTTTATAAT	AGACTAGCCA	CACTTCACTC	TGAAGAATTA	TTTATCCTTC	1986
AACAAGCATA	AATATTGCTG	TCAGAGAAGG	TTTTCATTTT	CATTTTTAAA	GATCTAGTTA	2046
ATTAAGGTGG	AAAACATATA	TGCTAAACAA	AAGAAACATG	ATTTTTCTTC	CTTAAACTTG	2106
AACACCAAAA	AACACACACA	CACACACA	CGTGGGGATA	GCTGGACATG	TCAGCATGTT	2166
AAGTAAAAGG	AGAATTTATG	AAATAGTAAT	GCAATTCTGA	TATCTTCTTT	CTAAAATTCA	2226
AGAGTGCAAT	TTTG					2240

(2) INFORMATION FOR SEQ ID NO:2:

- . (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn 1 5 10 15

Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe 20 25 30

Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu 35 40 45

Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys 50 55 60

Gln Thr Glu Cys Gly His Arg Ser Cys Glu Ser Cys Met Ala Ala Leu 65 70 75 80

Leu Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val 85 90 95

Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala

Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu 115 120 125

Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu 130 135 140

Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys 145 150 155 160

Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr 165 170 175

Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His

Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys 195 200 205

Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr Asn Gln Gln Ile Lys 210 225 220

Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu Leu Lys Glu 240

Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Lys Val Glu 255

Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser 260

Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu 275 280 285

Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys 290 295 300

Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe Arg Gln Asn Trp Glu 305 310 315 320

Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val 325 330 335

Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn 340 345 350

Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser 355 360 365

Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe Gln Val Leu 370 375 380

Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr 385 390 395 400

Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr 405 410 415

Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
420 425 430

Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
435 440 445

Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro 450 455 460

Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg 470 475 480

Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe 485

Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe 500 505 510

Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr 515 520 525

Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro 530 540

(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: GGAATTCAAA AAGGTGGCCA AG	22
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
TGATCATCAC TGTCTCCT GCAC	24
(2) INFORMATION FOR SEQ ID NO:5:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
GGAATTCAAG GCCCCCCACC CCAAG	25
(2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
TGATCAACTC TCTTTGCCAT CCTC	24

(2) INFORMATION FOR SEQ ID NO:7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
GGAATTCAAG AGAAAGGAAG TACAG (2) INFORMATION FOR SEQ ID NO:8:	25
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
GTGATCACTA GACCAAGCTT TGGAT	25
(2) INFORMATION FOR SEQ ID NO:9:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
GGAATTCAAA AAGAAGCCCT TGTGCCT	: 27
(2) INFORMATION FOR SEQ ID NO:10:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
GGTCGACTTA ACTGGGCTTC ATCCCA	26

٠.4

(2) INFORMATION FOR SEQ ID NO:11:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
GGGATCCGCT ACCAACGGTG GAAG	24
(2) INFORMATION FOR SEQ ID NO:12:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
GGTCGACTCA TCTGAGAAGA CTGGG	25
(2) INFORMATION FOR SEQ ID NO:13:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 54 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
TAATACGACT CACTATAGGG AGACCACATG GATGATGTAT ATAACTATCA TTTC	54
(2) INFORMATION FOR SEQ ID NO:14:	34
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
CTACCAGAAT TCGGCATGCC GGTAGAGGTG TGGTCA	36

(2)	INFORMATION FOR SEQ ID NO:15:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GCG:	TTAACTG CTCTGCACAA	20
(2)	INFORMATION FOR SEQ ID NO:16:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
GTA	CATTTTG GACTTGAAGA	20
(2)	INFORMATION FOR SEQ ID NO:17:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GAA	TTCCCGG GGATCCGTCG ACCTGCAG	28